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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Tue Nov 06 15:07:33 EST 2007

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Application No: 10553137

Version No: 1.0

Input Set:

Output Set:

Started: 2007-10-22 12:50:40.492

Finished: 2007-10-22 12:50:41.856

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 364 ms

Total Warnings: 0

Total Errors: 6

No. of SeqIDs Defined: 105

Actual SeqID Count: 105

Error code	Error Description
E 310	Invalid sequence type in <212> in SEQID: (1)
E 310	Invalid sequence type in <212> in SEQID: (2)
E 310	Invalid sequence type in <212> in SEQID: (3)
E 310	Invalid sequence type in <212> in SEQID: (4)
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SEQUENCE LISTING

<110> Berinstein, Neil
Gallichan, Scott
Lovitt, Corey
Parrington, Mark
Pedyczak, Artur
Radvanyi, Laszlo
Singh-Sandhu, Devender

<120> Tumor Antigens BFA5 for Prevention and/or Treatment of
Cancer

<130> API-03-03-PCT-US

<140> 10553137

<141> 2007-10-22

<150> PCT/IB2004/001701

<151> 2004-04-15

<150> US 60/462,945

<151> 2003-04-15

<160> 105

<170> PatentIn version 3.2

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<212> DNA (BFA4 cDNA)

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 <213> Homo sapiens

<400> 2

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35 40 45

Ser Asp Ala Ala Glu Leu Asn His Lys Glu Glu His Ser Leu His Val
50 55 60

Gln Asp Pro Ser Ser Ser Ser Lys Lys Asp Leu Lys Ser Ala Val Leu
65 70 75 80

Ser Glu Lys Ala Gly Phe Asn Tyr Glu Ser Pro Ser Lys Gly Gly Asn
85 90 95

Phe Pro Ser Phe Pro His Asp Glu Val Thr Asp Arg Asn Met Leu Ala
100 105 110

Phe Ser Phe Pro Ala Ala Gly Gly Val Cys Glu Pro Leu Lys Ser Pro
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Gln Arg Ala Glu Ala Asp Asp Pro Gln Asp Met Ala Cys Thr Pro Ser
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Gly Asp Ser Leu Glu Thr Lys Glu Asp Gln Lys Met Ser Pro Lys Ala
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Thr Glu Glu Thr Gly Gln Ala Gln Ser Gly Gln Ala Asn Cys Gln Gly
165 170 175

Leu Ser Pro Val Ser Val Ala Ser Lys Asn Pro Gln Val Pro Ser Asp
180 185 190

Gly Gly Val Arg Leu Asn Lys Ser Lys Thr Asp Leu Leu Val Asn Asp
195 200 205

Asn Pro Asp Pro Ala Pro Leu Ser Pro Glu Leu Gln Asp Phe Lys Cys
210 215 220

Asn Ile Cys Gly Tyr Gly Tyr Tyr Gly Asn Asp Pro Thr Asp Leu Ile
225 230 235 240

Lys His Phe Arg Lys Tyr His Leu Gly Leu His Asn Arg Thr Arg Gln
245 250 255

Asp Ala Glu Leu Asp Ser Lys Ile Leu Ala Leu His Asn Met Val Gln
260 265 270

Phe Ser His Ser Lys Asp Phe Gln Lys Val Asn Arg Ser Val Phe Ser
275 280 285

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290 295 300

Thr Tyr Asp Val Gln Val Thr Ser Gly Gly Thr Phe Ile Gly Ile Gly
305 310 315 320

Arg Lys Thr Pro Asp Cys Gln Gly Asn Thr Lys Tyr Phe Arg Cys Lys
325 330 335

Phe Cys Asn Phe Thr Tyr Met Gly Asn Ser Ser Thr Glu Leu Glu Gln
340 345 350

His Phe Leu Gln Thr His Pro Asn Lys Ile Lys Ala Ser Leu Pro Ser
355 360 365

Ser Glu Val Ala Lys Pro Ser Glu Lys Asn Ser Asn Lys Ser Ile Pro
370 375 380

Ala Leu Gln Ser Ser Asp Ser Gly Asp Leu Gly Lys Trp Gln Asp Lys
385 390 395 400

Ile Thr Val Lys Ala Gly Asp Asp Thr Pro Val Gly Tyr Ser Val Pro
405 410 415

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Tyr Tyr Trp Cys Lys Phe Cys Ser Phe Ser Cys Glu Ser Ser Ser Ser
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Ile	Lys	His	Cys	Pro	Phe	Cys	Pro	Arg	Gly	Leu	Cys	Ser	Pro	Glu	Lys	565	570	575
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Ser	Ser	Arg	Val	Lys	His	Gln	Cys	His	Gln	Cys	Ser	Phe	Thr	Thr	Pro	610	615	620
Asp	Val	Asp	Val	Leu	Leu	Phe	His	Tyr	Glu	Ser	Val	His	Glu	Ser	Gln	625	630	635
Ala	Ser	Asp	Val	Lys	Gln	Glu	Ala	Asn	His	Leu	Gln	Gly	Ser	Asp	Gly	645	650	655
Gln	Gln	Ser	Val	Lys	Glu	Ser	Lys	Glu	His	Ser	Cys	Thr	Lys	Cys	Asp	660	665	670

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725 730 735

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755 760 765

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805 810 815

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820 825 830

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835 840 845

Thr Lys Gly Phe Leu Gln Gly Ala Pro Ala Gly Gly Glu Lys Ser Gly
850 855 860

Ala Leu Pro Gln Gln Tyr Pro Ala Ser Gly Glu Asn Lys Ser Lys Asp
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Ala Asn Cys Leu Thr Thr Lys Thr Ser Leu Trp Arg Lys Asn Ala Asn

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